

SEQUENCE LISTINGS

<110> INJE UNIVERSITY

<120> CANCER CELL TARGETING GENE DELIVERY METHOD

<130> PCA31275/IJU

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<170> KopatentIn 1.71

<210> 1

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Env F primer

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36

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<211> 47

<212> DNA

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<223> 597LN primer

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<211> 49

<212> DNA

<213> Artificial Sequence

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<223> LC597 primer

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caaccccgcc gcaggtggag gaggcagtga atggactcaa aaatttcaa

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DNA

<213>

Artificial Sequence

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<223> Spike R2 primer

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35

<210>

5

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DNA

<213>

Artificial Sequence

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<223> LnkNScFv primer

<400> 5

ggaggtggtg gcagccaggt ccagctagtg cagtct

36

<210>

6

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DNA

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Artificial Sequence

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<223> ScFvLnkC primer

<400>

6

actgcctcct ccacctgcgg cgggggttgaa gtccca

36

<210> 7
 <211> 2058
 <212> DNA
 <213> SEAT0 type of GaLV Env glycoprotein

<220>
 <221> sig_peptide
 <222> (1)..(126)

<220>
 <221> misc_feature
 <222> (127)..(1467)
 <223> surface subunit region

<220>
 <221> misc_feature
 <222> (1468)..(2025)
 <223> transmembrain domain

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 gggacgagtc tgcaaaataa gaacccccac cagcccatga cctcacttg gcaggctactg 180
 tcccaaactg gagacgttgt ctgggataca aaggcagtc agcccccttg gacttggtgg 240
 cccacactta aacctgatgt atgtgccttg gcggtagtc ttgagtcctg ggatatcccg 300
 ggaaccgatg tctcgtctc taaacgagtc agacctcgg actcagacta tactgccgct 360
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 gcaagctcta ccttctacgt atgtccccgg gatggccgga ccctttcaga agctagaagg 480
 tgcggggggc tagaatccct atactgtaaa gaatgggatt gtgagaccac ggggaccggt 540
 tattggctat ctaaatctc aaaagacctc ataactgtaa aatgggacca aaatagcgaa 600

tggactcaaa aatttcaaca gtgtcaccag accggctggt gtaaccccct taaaatagat	660
ticacagaca aaggaaaaai aiccaaggac iggaiaacgg gaaaaacctg gggattaaga	720
ttctatgtgt ctggacatcc aggcgtacag ttcaccattc gcttaaaaat caccaacatg	780
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gaagagtgct gtttttcat agaccactca ggtgcagtac gggactccat gaaaaaactc	1800
aaagaaaaac tggataaaag acagtttagag cgccagaaaa gccaaaactg gtatgaagga	1860
tggttcaata actccccttg gttaactacc ctgctatcaa ccctcgtgg gccctatta	1920

ctctctcttc tgttgctcat cctcggggcca tgcatcatca ataagttagt tcaattcatc 1980
 aatgatagga taagtgcagt taaaattctg gtccttagac aaaaatatca ggccctagag 2040
 aacgaaggta acctttaa 2058

<210> 8
 <211> 786
 <212> DNA
 <213> Tag-72pS1

<220>
 <221> misc_feature
 <222> (346)..(390)
 <223> (Gly4Ser)3 linker

<220>
 <221> misc_feature
 <222> (739)..(777)
 <223> PreS1 Tag

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 cctggacaac gccttgagtg gatgggatat tttctcctg gcaacgatga ttttaaatac 180
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 ctggctgtgt ctctgggcga gagggccacc atcaactgca agtccagcca gagtgttta 480
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aagctgctca ttactgggc atctaccogg gaatccgggg tccctgaccg attcagtggc 600
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 gtttattact gtcagcaata ttattcctat ccgttgacgt tcggccaagg gaccaagggt 720
 gaaatcaaag cggccgcagg agccaacgca aacaatccag attgggactt caaccccgcc 780
 gcatag 786

<210> 9
 <211> 13
 <212> PRT
 <213> PreS1 epitope at C-terminal of Tag-72pS1

<400> 9
 Gly Ala Asn Ala Asn Asn Pro Asp Trp Asp Phe Asn Pro
 1 5 10

<210> 10
 <211> 2871
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ScFv-GaLV Env GP chimeric peptide (FvGEL199) DNA

<400> 10
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caaactccca cggtagagaaa aacaattggt accctaaaca ctccgcctcc caccacaggc 1800
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 gagcgccaga aaagccaaaa ctggtatgaa ggatggttca ataactcccc ttggttcaact 2700
 accctgctat caaccatcgc tggggcccta ttactcctcc ttctgttgct catcctcggg 2760
 ccatgcatca tcaataagtt agttcaattc atcaatgata ggataagtgc agttaaatt 2820
 ctggtcctta gacaaaaata tcaggcccta gagaacgaag gtaaccttta a 2871

<210> 11
 <211> 956
 <212> PRT
 <213> Artificial Sequence

<220>

<223> ScFv-GaLV Env GP chimeric ligand (FvGEL199)

<400> 11

Met Val Leu Leu Pro Gly Ser Met Leu Leu Thr Ser Asn Leu His His
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Leu Arg His Gln Met Ser Pro Gly Ser Trp Lys Arg Leu Ile Ile Leu
 20 25 30

Leu Ser Cys Val Phe Gly Gly Gly Gly Thr Ser Leu Gln Asn Lys Asn
 35 40 45

Pro His Gln Pro Met Thr Leu Thr Trp Gln Val Leu Ser Gln Thr Gly
 50 55 60

Asp Val Val Trp Asp Thr Lys Ala Val Gln Pro Pro Trp Thr Trp Trp
 65 70 75 80

Pro Thr Leu Lys Pro Asp Val Cys Ala Leu Ala Ala Ser Leu Glu Ser
 85 90 95

Trp Asp Ile Pro Gly Thr Asp Val Ser Ser Ser Lys Arg Val Arg Pro
 100 105 110

Pro Asp Ser Asp Tyr Thr Ala Ala Tyr Lys Gln Ile Thr Trp Gly Ala
 115 120 125

Ile Gly Cys Ser Tyr Pro Arg Ala Arg Thr Arg Met Ala Ser Ser Thr
 130 135 140

Phe Tyr Val Cys Pro Arg Asp Gly Arg Thr Leu Ser Glu Ala Arg Arg
 145 150 155 160

Cys Gly Gly Leu Glu Ser Leu Tyr Cys Lys Glu Trp Asp Cys Glu Thr
 165 170 175

Thr Gly Thr Gly Tyr Trp Leu Ser Lys Ser Ser Lys Asp Leu Ile Thr
 180 185 190

Val Lys Trp Asp Gln Asn Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
 195 200 205

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 210 215 220

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His Ala Ile His Trp
 225 230 235 240

Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Tyr Phe Ser
 245 250 255

Pro Gly Asn Asp Asp Phe Lys Tyr Ser Gln Lys Phe Gln Gly Arg Val
 260 265 270

Thr Ile Thr Ala Asp Lys Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser
 275 280 285

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu
 290 295 300

Asp Met Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
 305 310 315 320

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
 325 330 335

Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg
 340 345 350

Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn
 355 360 365

Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 370 375 380

Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp
 385 390 395 400

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 405 410 415

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr
 420 425 430

Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ala

435		440		445
Ala Ala Gly Ala Asn Ala Asn Asn Pro Asp Trp Asp Phe Asn Pro Ala	450	455	460	
Ala Gly Gly Gly Gly Ser Glu Trp Thr Gln Lys Phe Gln Gln Cys His	465	470	475	480
Gln Thr Gly Trp Cys Asn Pro Leu Lys Ile Asp Phe Thr Asp Lys Gly	485	490	495	
Lys Leu Ser Lys Asp Trp Ile Thr Gly Lys Thr Trp Gly Leu Arg Phe	500	505	510	
Tyr Val Ser Gly His Pro Gly Val Gln Phe Thr Ile Arg Leu Lys Ile	515	520	525	
Thr Asn Met Pro Ala Val Ala Val Gly Pro Asp Leu Val Leu Val Glu	530	535	540	
Gln Gly Pro Pro Arg Thr Ser Leu Ala Leu Pro Pro Pro Leu Pro Pro	545	550	555	560
Arg Glu Ala Pro Pro Pro Ser Leu Pro Asp Ser Asn Ser Thr Ala Leu	565	570	575	
Ala Thr Ser Ala Gln Thr Pro Thr Val Arg Lys Thr Ile Val Thr Leu	580	585	590	
Asn Thr Pro Pro Pro Thr Thr Gly Asp Arg Leu Phe Asp Leu Val Gln	595	600	605	
Gly Ala Phe Leu Thr Leu Asn Ala Thr Asn Pro Gly Ala Thr Glu Ser	610	615	620	
Cys Trp Leu Cys Leu Ala Met Gly Pro Pro Tyr Tyr Glu Ala Ile Ala	625	630	635	640
Ser Ser Gly Glu Val Ala Tyr Ser Thr Asp Leu Asp Arg Cys Arg Trp	645	650	655	
Gly Thr Gln Gly Lys Leu Thr Leu Thr Glu Val Ser Gly His Gly Leu	660	665	670	

Cys Ile Gly Lys Val Pro Phe Thr His Gln His Leu Cys Asn Gln Thr
675 680 685

Leu Ser Ile Asn Ser Ser Gly Asp His Gln Tyr Leu Leu Pro Ser Asn
690 695 700

His Ser Trp Trp Ala Cys Ser Thr Gly Leu Thr Pro Cys Leu Ser Thr
705 710 715 720

Ser Val Phe Asn Gln Thr Arg Asp Phe Cys Ile Gln Val Gln Leu Ile
725 730 735

Pro Arg Ile Tyr Tyr Tyr Pro Glu Glu Val Leu Leu Gln Ala Tyr Asp
740 745 750

Asn Ser His Pro Arg Thr Lys Arg Glu Ala Val Ser Leu Thr Leu Ala
755 760 765

Val Leu Leu Gly Leu Gly Ile Thr Ala Gly Ile Gly Thr Gly Ser Thr
770 775 780

Ala Leu Ile Lys Gly Pro Ile Asp Leu Gln Gln Gly Leu Thr Ser Leu
785 790 795 800

Gln Ile Ala Ile Asp Ala Asp Leu Arg Ala Leu Gln Asp Ser Val Ser
805 810 815

Lys Leu Glu Asp Ser Leu Thr Ser Leu Ser Glu Val Val Leu Gln Asn
820 825 830

Arg Arg Gly Leu Asp Leu Leu Phe Leu Lys Glu Gly Gly Leu Cys Ala
835 840 845

Ala Leu Lys Glu Glu Cys Cys Phe Tyr Ile Asp His Ser Gly Ala Val
850 855 860

Arg Asp Ser Met Lys Lys Leu Lys Glu Lys Leu Asp Lys Arg Gln Leu
865 870 875 880

Glu Arg Gln Lys Ser Gln Asn Trp Tyr Glu Gly Trp Phe Asn Asn Ser
885 890 895

Pro Trp Phe Thr Thr Leu Leu Ser Thr Ile Ala Gly Pro Leu Leu Leu
900 905 910

Leu Leu Leu Leu Leu Ile Leu Gly Pro Cys Ile Ile Asn Lys Leu Val
915 920 925

Gln Phe Ile Asn Asp Arg Ile Ser Ala Val Lys Ile Leu Val Leu Arg
930 935 940

Gln Lys Tyr Gln Ala Leu Glu Asn Glu Gly Asn Leu I
945 950 955